MULTIMEDIA UNIVERSITY®

STUDENT ID NO

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# MULTIMEDIA UNIVERSITY

# FINAL EXAMINATION

**TRIMESTER 2, 2016/2017**

## HPB2011 – BIOINFORMATICS PROGRAMMING I

(All sections / Groups)

10- March- 2017
03:00-05:00 PM
(2 Hours)

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**INSTRUCTIONS TO STUDENTS**

1. This question paper consists of 6 pages including cover page and 4 questions only.

2. Attempt all **FOUR** questions. All questions carry equal marks (10), and the distribution of the marks for each question is given.

3. Please write all your answers in the Answer Booklet provided

## QUESTION 1 [10 marks]

a. Briefly explain pairwise sequence alignment and list two categories of sequence pairwise alignment. What are the two applications of pairwise sequence alignment? [2 marks]

b. What are some of the differences between the Chou-Fasman and the GOR methods for estimating secondary structures? [2 marks]

c. Given the following part of the Chou-Fasman table,

| Name | | P(a) | P(b) | P(turn) |
|---|---|---|---|---|
| Ala | A | 142 | 83 | 66 |
| Cys | C | 70 | 119 | 119 |
| Asp | D | 101 | 54 | 146 |
| Glu | E | 151 | 37 | 74 |
| Phe | F | 113 | 138 | 60 |
| Gly | G | 57 | 75 | 156 |
| His | H | 100 | 87 | 95 |
| Iso | I | 108 | 160 | 47 |
| Lys | K | 114 | 74 | 101 |
| Leu | L | 121 | 130 | 59 |
| Met | M | 145 | 105 | 60 |
| Asn | N | 67 | 89 | 156 |
| Pro | P | 57 | 55 | 152 |
| Gln | Q | 111 | 110 | 98 |
| Arg | R | 98 | 93 | 95 |
| Ser | S | 77 | 75 | 143 |
| Thr | T | 83 | 119 | 96 |
| Val | V | 106 | 170 | 50 |

| | | | | |
|---|---|---|---|---|
| Try | W | 108 | 137 | 96 |
| Tyr | Y | 69 | 147 | 114 |

calculate the secondary structure of the following sequence, only for α-helices and β-sheets (not for turns): R G P T C W P A E N K L . Give your answer as a table [6 marks]

**Continued....**

## QUESTION 2 [10 marks]

a. Write a java class PdbReader to read a PDB file and store the sequence in a String variable. Declare at least 4 instance attributes for PdbReader class. Two attributes to **read** the PDB file and **buffer** the content and two attributes for **name of the file** ("5LZM.PDB") and the extracted **sequence**. Do not forget to import the suitable package to read a file. [3 marks]

b. Write a function; **readPDBfile()**, to instantiate the attributes and read the file line by line to extract the sequence from the lines which start with "**SEQRES**". Sequence is located between the positions 18 to 72 of every line. Append the extracted sequence from each line to the String variable you declared for the sequence in part a. Do not forget to use the required **exception handling**. [6 marks]

c. Write a part of code for class PdbReader to declare an Arraylist and split the long String sequence using space delimiter to be assigned to the Arraylist. [1 mark]

**Continued....**

**QUESTION 3 [10 marks]**

a. Declare and define a java static function *reverse_complement(seq)* that returns the reverse complement of input sequence *seq*. Declare an Arraylist and add the complement of every base to it. Define a control system to check all bases should be among "a","t","c", and "g", otherwise it produces an error massage. [5 marks]
(Hint: you may use the Collection package to obtain the reverse form of the sequence.)

- complement_map = {'c': 'g', 'g': 'c', 'a': 't', 't': 'a'}
- example seq=aaaccc; output=gggttt

b. Letters (A T G C) can be used to describe a DNA gene in the form of string of letters. A sequence also can be described as codons – 3-letter 'words', each of which corresponds to an amino acid (or a stop codon).

Write a Java class "Codons" and declare two attributes as data members, a variable for sequence and an array or arraylist to store the codons. Define a constructor to instantiate the data members. Also define a function getSequence() to return the value of "sequence" attribute. [2.5 marks]

c. For Codon class in part b write a Java method readFrames() to fill the arraylist (or array) with the codons from sequence starting with the first letter in the sequence. Ignore codons which have <3 letters at the end of seq. Loop through each ArrayList (or array) and print the codons as a list. [2.5 marks]

**Continued....**

**QUESTION 4 [10 marks]**

a. Explain at least two differences between function overloading and function overriding in Java Programming with an example. [3 marks]

b. There is an underlying class named "Conductance" to contain the common material for the leak, calcium and potassium conductance. Each of these has a maximum conductance ("maxc") and an equilibrium potential ("equilibrium"), both double numbers. Write an Abstract class Conductance with "maxc" and "equilibrium" data members. The abstract class has a method called current which receives the value of potential (a double number) and returns the value of current using the following formula:

```
Conductance = maxc * potential
Current = conductance * (potential – equilibrium)
```

The abstract class has also an abstract function "permeability" that is a portion of conductance we achieved. This method receives a double variable as "potential". [3 marks]

c. Write a subclass for part b called "LeakConductance" in which permeability method returns the value 1.0. [1 mark]

d. Write another subclass for part b called CalciumConductance which has two additional parameters v1 and v2 and a constructor to initialize all parameters including v1 and v2. The permeability for CalciumConductance can be calculated using the following formula: [3 marks]

```
transformed = (potential –v1) / v2;
permeability = 0.5 * (1 + Math.tanh(transformed));
```

**End of Paper**